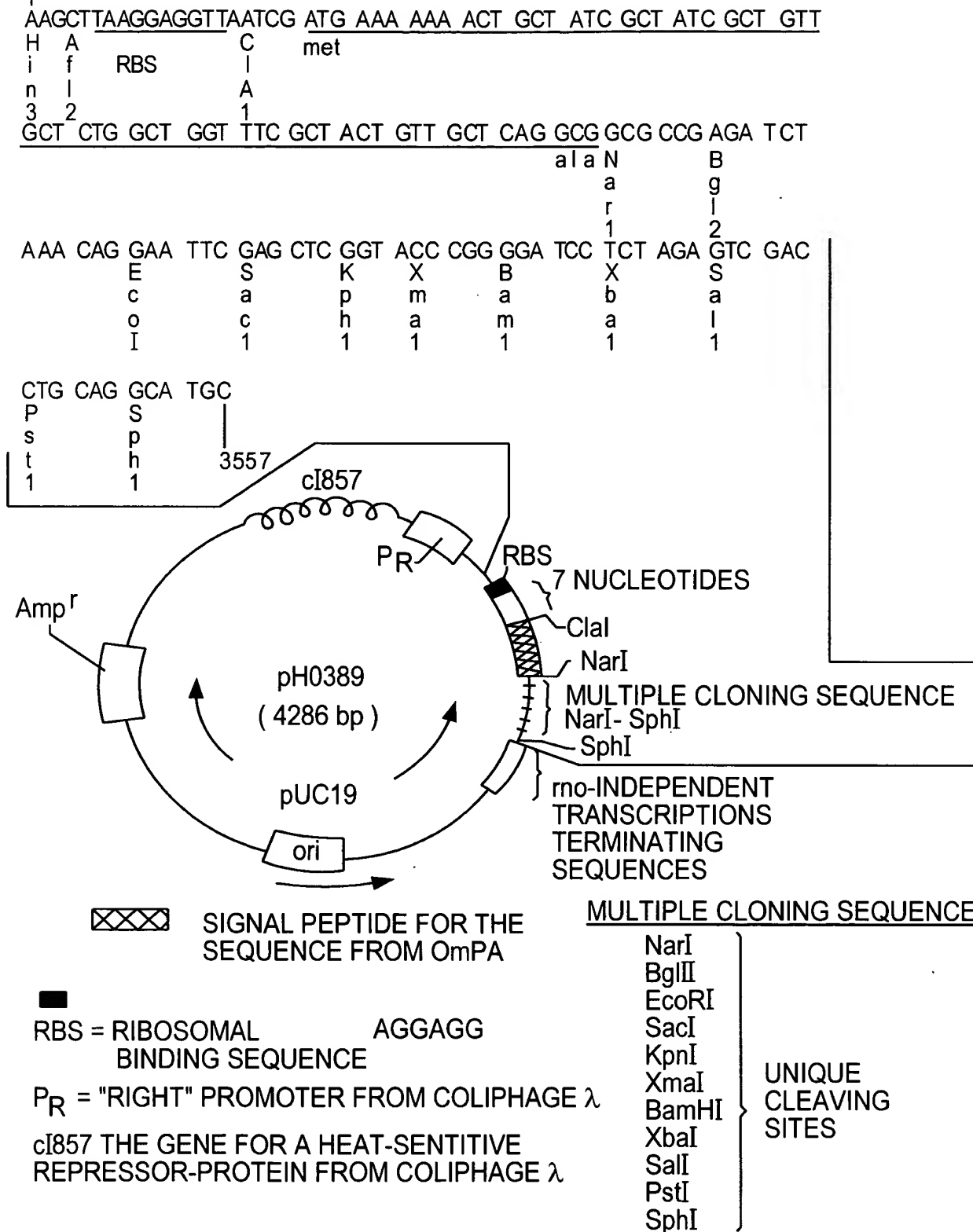




FIG. 1



PLASMA pH0389. THE RIBOSOMAL BINDING-SEQUENCE (EMPHASIZED WITH A FULL LINE), THE SEQUENCE FOR SIGNAL PEPTIDE FROM ompA (FROM E.coli) (DOTTED LINE) AND RECOGNITION SEQUENCE FOR SEVERAL RESTRICTION ENZYMES ARE SHOWN.

ACAATCAAAGCTAACCTAA^VCTTTGCAAAATGGAAGCACACAAACTGCAGAA^VTTCAAAGGA^V
Th r I l e L y s A l a A s n L e u I l e P h e A l a A s n G l y S e r T h r G l n T h r A l a G l u P h e L y s G l y

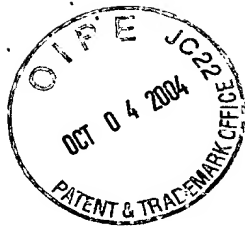
ACATTGAAAAAGCAACATCAGAAGCTTATGCGTATGCAGATACTTTGAAGAAAGACAAT^V
ThrPheGluLysAlaThrSerGluAlaTyrAlaTyrAlaAspThrLeuLysLysAspAsn^V

GGAGAATA TACTGTAGATGT TGCAGATA AAGGTTAT TACTTTAAATATTTAAATTTTGCTGGA^V
GlyGluTrpThrValAspValAlaAspLysGlyTyrThrLeuAsnIleLysPheAlaGly^V

GCAGATGGAAAAACACAAACAGCAGAA^VTTCAAGGAACAT^VTTGAAGAAGCAACAGCAGAA^V
AlaAspGlyLysThrGlnThrAlaGluPheLysGlyThrPheGluGluAlaThrAlaGlu^V

PROTEIN LG

FIG. 2b



GCATACAGATATGCAGATGCATTAAAGAAAGGACAATGGAGAAATATACAGTAGACGTTGCA
AlaTyrArgTyrAlaAspAlaLeuLysLysAspAsnGlyGluTyrThrValAspValAla
420
140

GATAAAGGTTACTTTTAAATATTAAATTTGCTGGAAAGAAAAACACCAGAAAGAACCA
AspLysGlyTyrThrLeuAsnIleLysPheAlaGlyLysGluLysThrProGluGluPro
480
160

AAAGAAGAAGTTACTATTAAAGCAAACTTAATCTATGCAGATGGAAAAACACAAACAGCA
LysGluGluValThrIleLysAlaAsnLeuIleTyrAlaAspGlyLysThrGlnThrAla
540
180

GATTCAAAGGAACATTTGAAGAAGCAACAGCAGAAGCATACAGATATGCTGACTTATTA
GluPheLysGlyThrPheGluGluAlaThrAlaGluAlaTyrArgTyrAlaAspLeuLeu
600
200

GCAAAAGAAAATGGTAAATATACAGTAGACGTTGCAGATAAAGGTTACTTTAAATATT
AlaLysGluAsnGlyLysTyrThrValAspValAlaAspLysGlyTyrThrLeuAsnIle
660
220

AAATTTGCTGGAAAAAACAACCCAGAAAGAACCAAGAGTTACTATTAAAGCA
LysPheAlaGlyLysGluLysThrProGluGluProLysGluGluValThrIleLysAla
720
240

AACTTAATCTATGCAGATGGAAAAACTCAACAGCAGAGTTCAAAGGAACATTTGCAGAA
AsnLeuIleTyrAlaAspGlyLysThrGlnThrAlaGluPheLysGlyThrPheAlaGlu
780
260

FIG. 2c

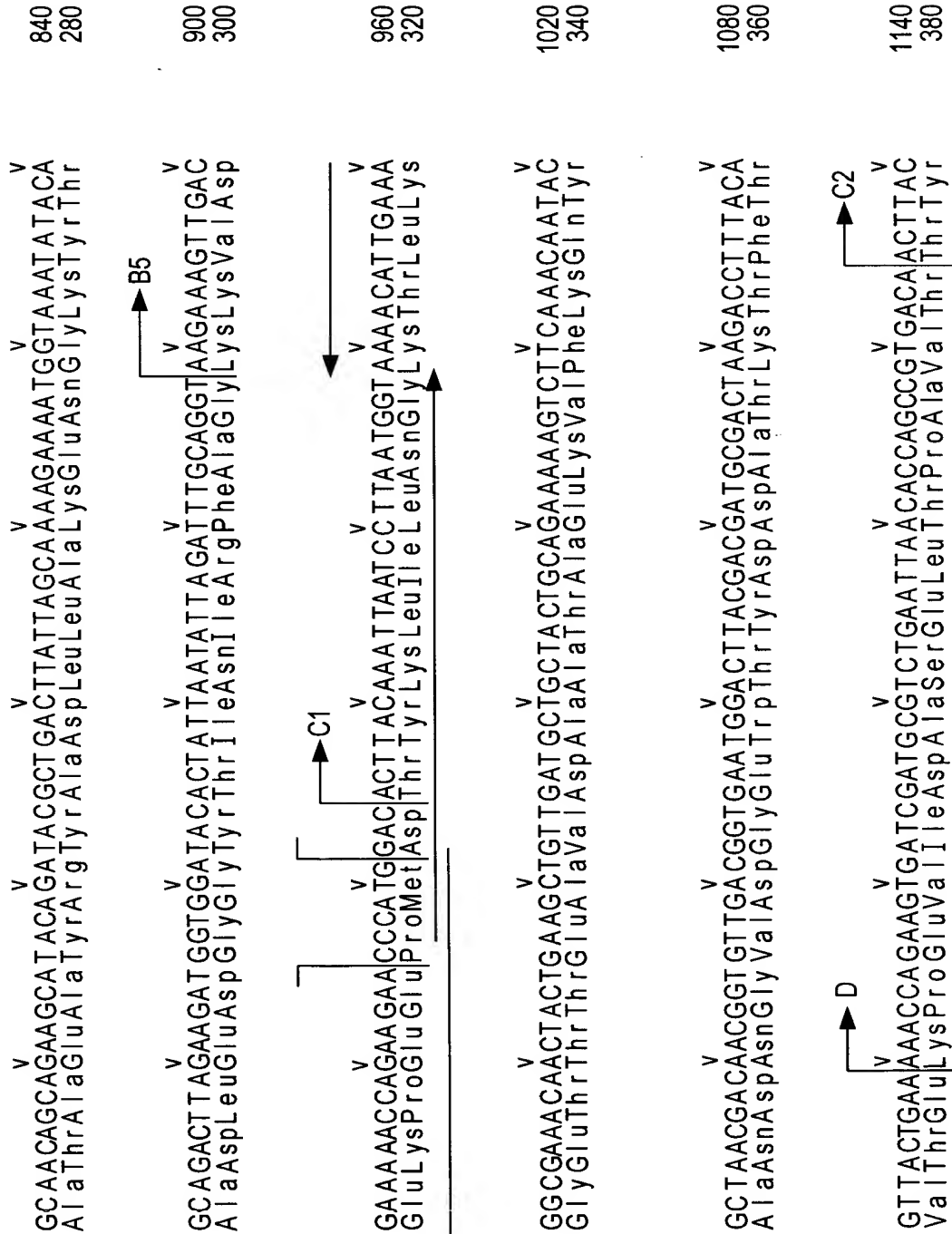


FIG. 2d



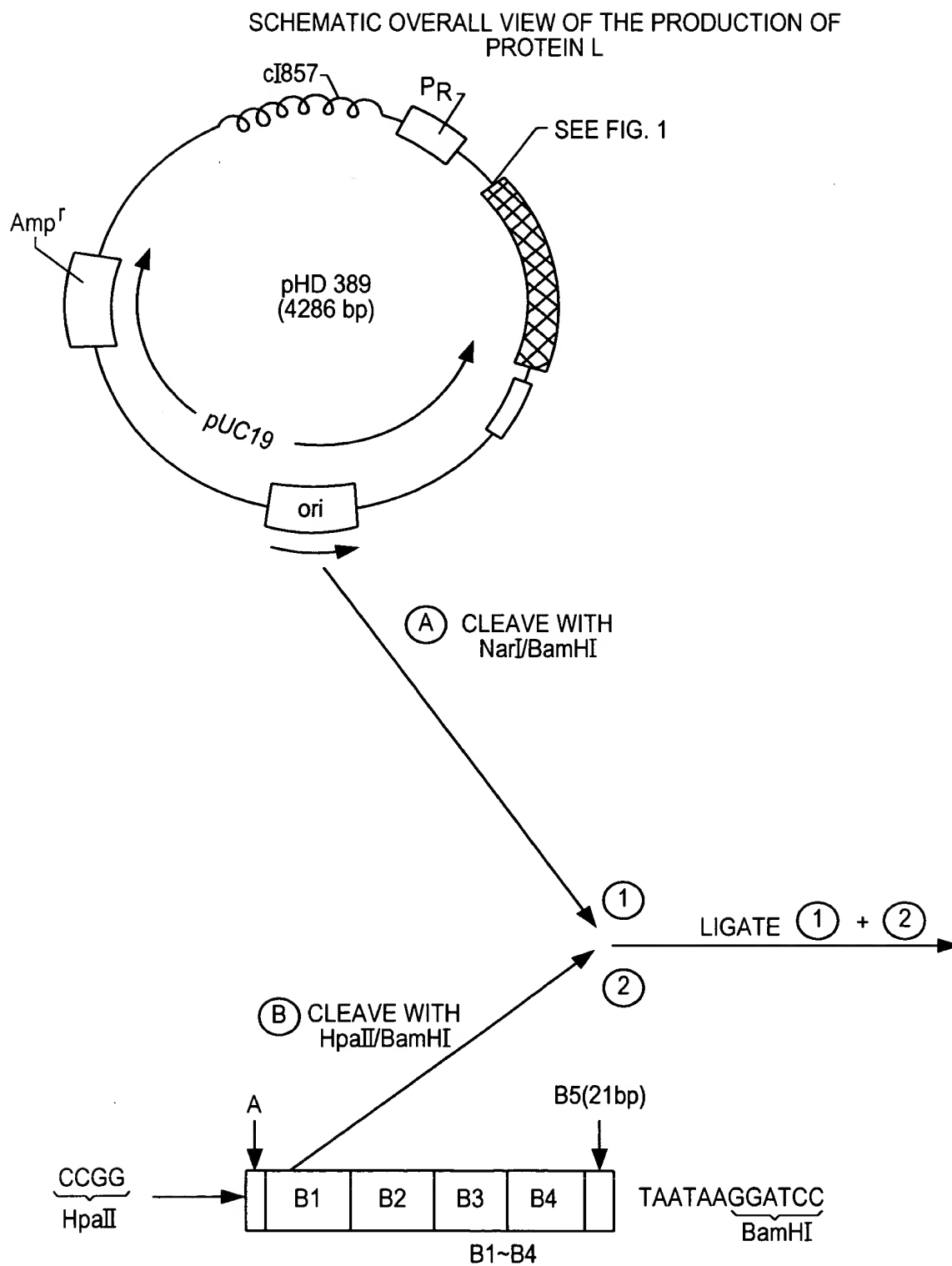
<div>AAACTTGTATTAAATGGTAAACACATTGAAAGCGGAAACAACTACTAAAGCAGTAGACGCA LysLeuValIleAsnGlyLysThrLeuLysGlyGluThrThrThrLysAlaValAspAla</div>	<div>1200 400</div>
<div>GAAACTGCAGAAAAAGCCTTCAAACAATACGCTAACGACAACGGTGTGATGGTGTGTTGG GluThrAlaGluLysAlaPheLysGlnTyrAlaAsnAspAsnGlyValAspGlyValTrp</div>	<div>1260 420</div>
<div>ACTTATGATGATGCGACTAAGACCTTTACGGTAACTGAAATGTATAATAA ThrTyrAspAspAlaThrLysThrPheThrValThrGluMet - -</div>	<div>1308 434</div>

FIG. 2e



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FIG. 3(1)



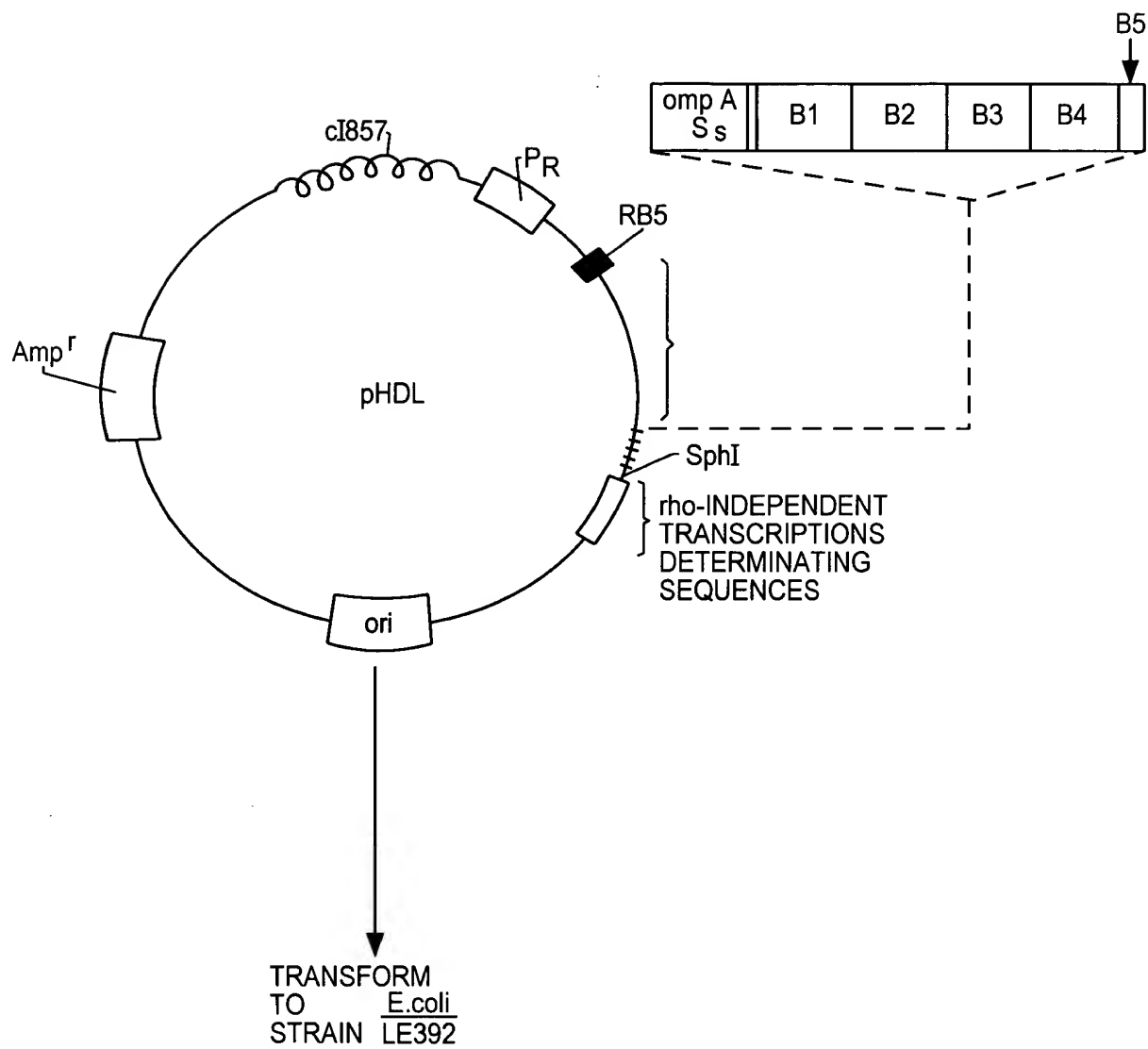


FIG. 3(2)

SCHEMATIC OVERALL VIEW OF PRODUCTION OF PROTEIN LG

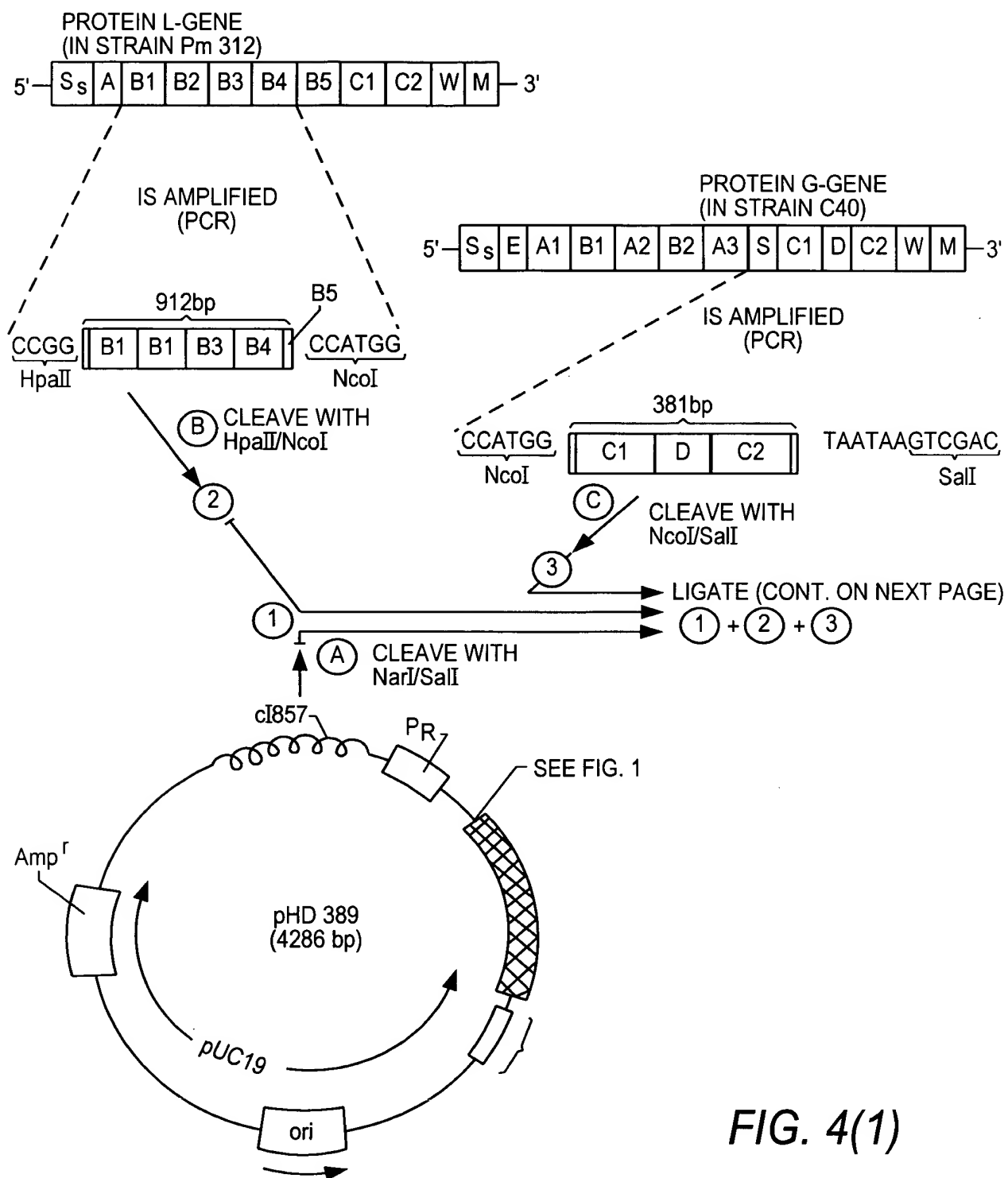


FIG. 4(1)



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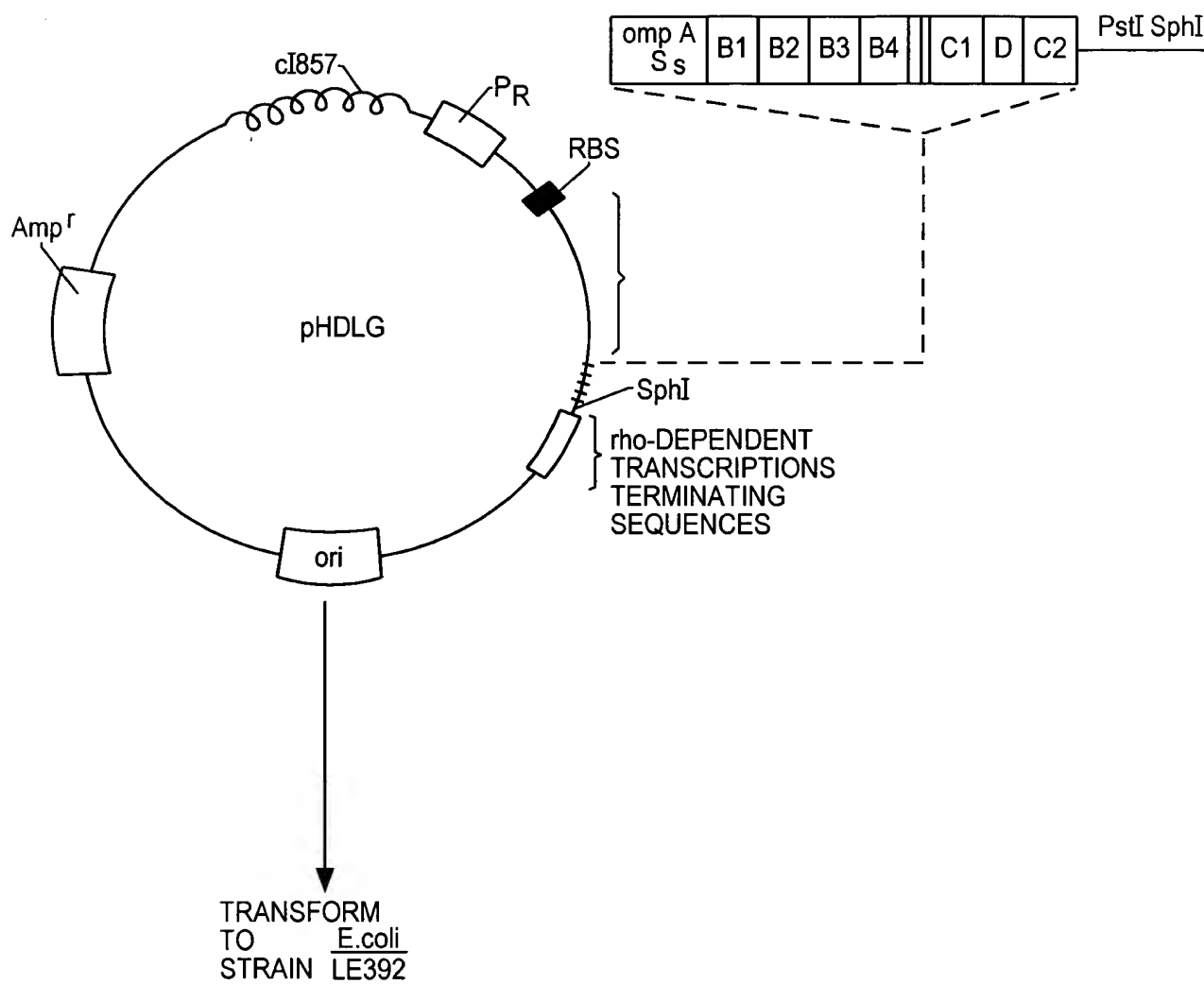


FIG. 4(2)



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SCHEMATIC OVERALL VIEW OF PRODUCTION OF PROTEIN LA

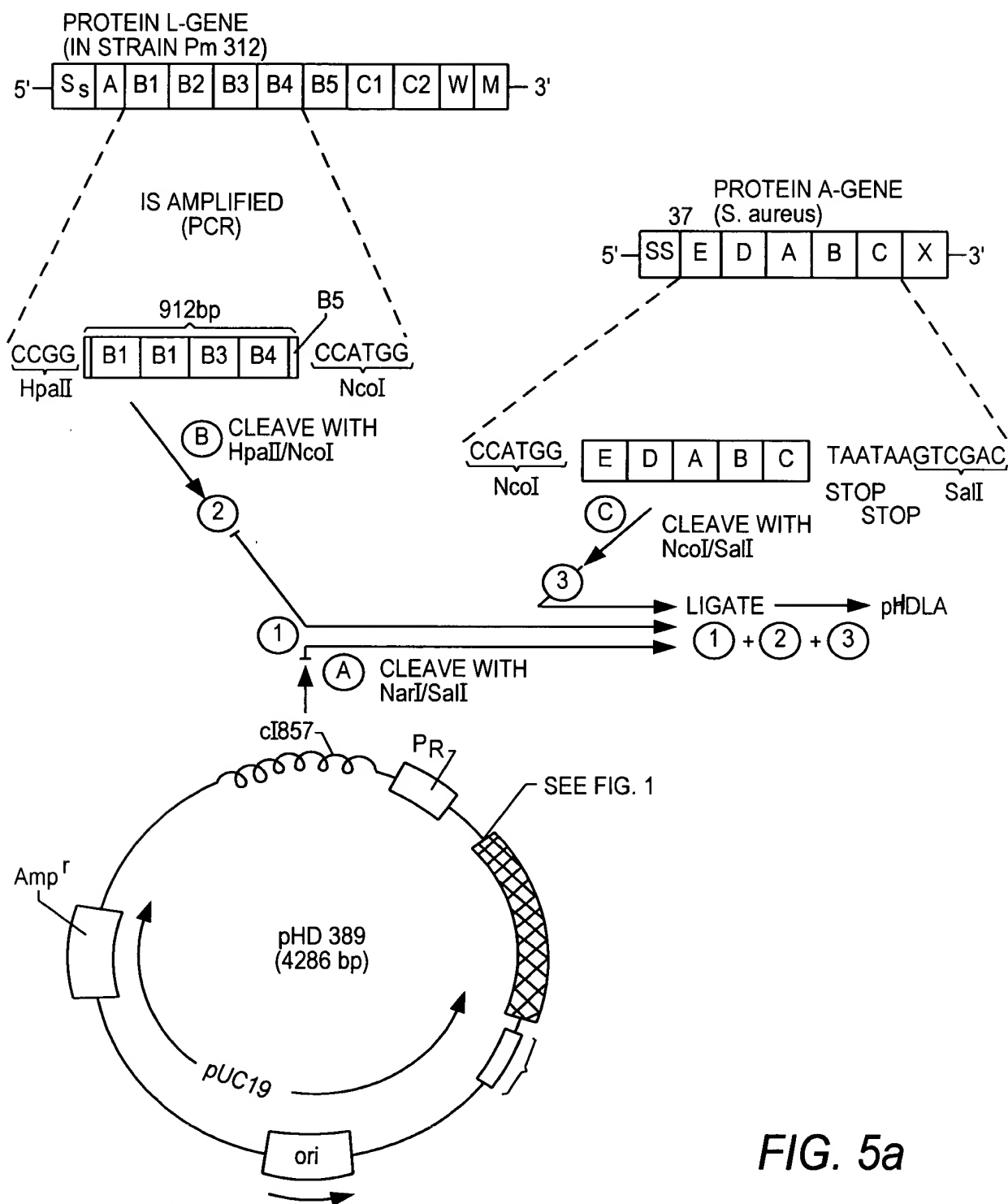


FIG. 5a

SCHEMATIC OVERALL VIEW OF PRODUCTION OF PROTEIN LM

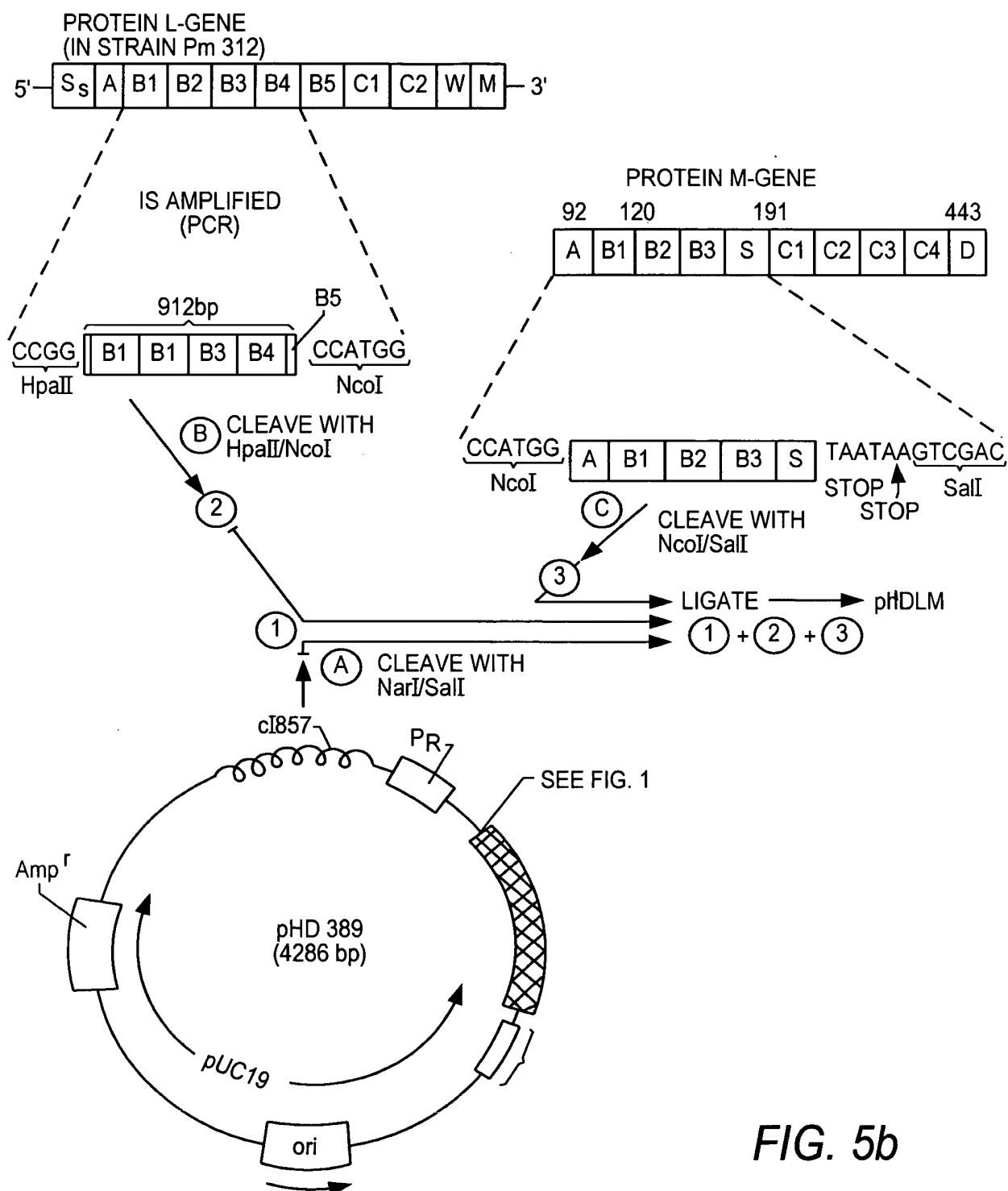


FIG. 5b

SCHEMATIC OVERALL VIEW OF PRODUCTION OF PROTEIN LH

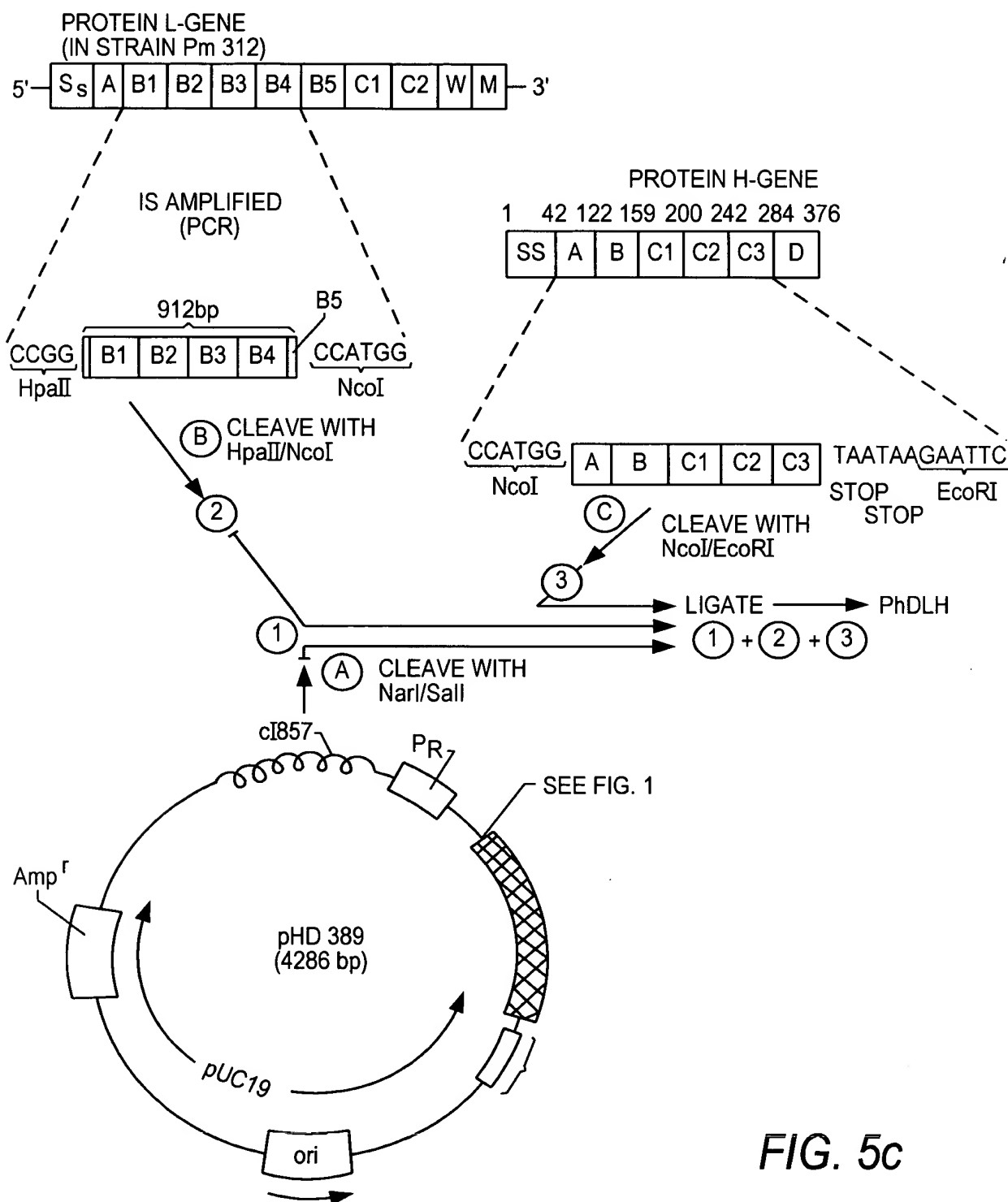
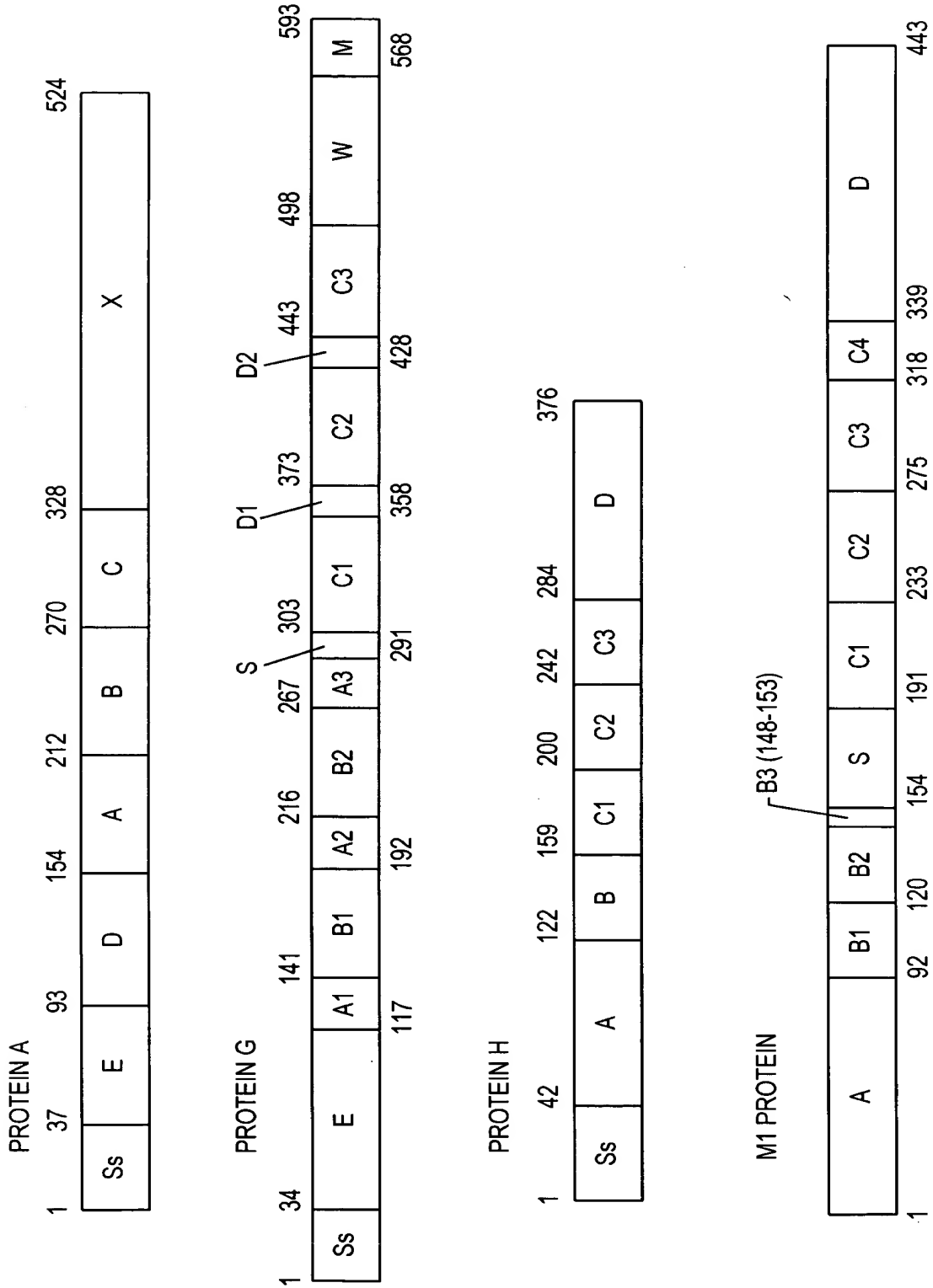


FIG. 5c





AACGGTGATGGTAATCCTAGGGAAGTTATAGAAAGATCTTGCAGCAAAACAATCCCGCAATA^V
AsnGlyAsoGlyAsnProArgGluValIleGluAspLeuAlaAlaAsnAsnFroAlaIle^V 60 20

CAAAATATACGTTTACGTCACGAAACAAAGGACTTAAAGCGAGATTAGAGAATGCAATG^V
GlnAsnIleArgLeuArgHisGluAsnLysAspLeuLysAlaArgLeuGluAsnAlaMet^V 120 40

GAAGTTGCAGGAAGAGATTTTAAGAGAGCTGAAGAACTTGAAAAAGCAAAACAAGCCTTA^V
GluValAlaGlyArgAspPheLysArgAlaGluGluLeuGluLysAlaLysGlnAlaLeu^V 180 60

GAAGACCAGCGTAAAGATTTAGAAACTAAATTAAAGAACTACAACAAGACTATGACTTA^V
GluAspGlnArgLysAspLeuGluThrLysLeuLysGluLeuGlnGlnAspTyrAspLeu^V 240 80

GCAAAAGGAATCAACAAGTTGGGATAGACAAAGACTTGAAAAAGAGTTAGAAGAGAAAAAG^V
AlaLysGluSerThrSerTrpAspArgGlnArgLeuGluLysGluLeuGluGluLysLys^V 300 100

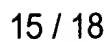
GAAGCTCTTGAATTAGCGATAGACCAAGCAAGTCGGGACTACCATAGAGCTACCGCTTTA^V
GluAlaLeuGluLeuAlaIleAspGlnAlaSerArgAspTyrHisArgAlaThrAlaLeu^V 360 120

GAAAAAGAGTTAGAAAGAGAAAAAGAAAGCTCTTGAATTAGCGATAGACCAAGCGAGTCAG^V
GluLysGluLeuGluGluLysLysAlaLeuGluLeuAlaIleAspGlnAlaSerGln^V 420 140

GACTATAATAGAGCTAACGTCTTAGAAAAAGAGTTAGAAACGATTACTAGAGAAACAAGAG^V
AspTyrAsnArgAlaAsnValLeuGluLysGluLeuGluThrIleThrArgGluGlnGlu^V 480 160

ATTAATCGTAATCTTTTAGGCAATGCAAAAACCTTGAACTTGATCAACTTTTCATCTGAAAAA^V
IleAsnArgAsnLeuLeuGlyAsnAlaLysLeuGluLeuAspGlnLeuSerSerGluLys^V 540 180

FIG.7a



AMINO ACID SEQUENCE AND NUCLEIC ACID SEQUENCE FOR PROTEIN M1, IgG-BINDING SOMEWHERE BETWEEN AMINO ACID 1-190.

FIG. 7b



840
280
900
300
960
320
1020
340
1080
360
1140
380
1200
400
1260
420
1320
440

G A A A A G A T T T A G C A A A C T T G A C T G C T G A A C T T G A T A A G G T T A A A G A A G A A A A C A A A T C
G l u L y s A s p L e u A l a A s n L e u T h r A l a G l u L e u A s p L y s V a l L y s G l u G l u L y s G l n I l e
T C A G A C G C A A G C C G T C A A C G G C T T C G C C G T G A C T T G G A C G C A T C A C G T G A A G C T A A G A A A
S e r A s p A l a S e r A r g G l n A r g L e u A r g A s p L e u A s p A l a S e r A r g G l u A l a L y s L y s
C A A G T T G A A A A G C T T T A G A A G A A G C A A A C A G C A A A T T A G C T G C T C T T G A A A A C T T A A C
G l n V a l G l u L y s A l a L e u G l u A l a A s n S e r L y s L e u A l a A l a L e u G l u L y s L e u A s n
A A G A G C T T G A A G A A A G C A A G A A T T A A C A G A A A A A A A G C T G A A C T A C A A G C A A A A
L y s G l u L e u G l u G l u S e r L y s L y s L e u T h r G l u L y s G l u L y s A l a G l u L e u G l n A l a L y s
C T T G A A G C A A G C A A A A G C A C T C A A A G A A C A A T T A G C G A A A C A A G C T G A A G A A C T C G C A
L e u G l u A l a G l u A l a L y s A l a L e u L y s G l u G l n L e u A l a L y s G l n A l a G l u G l u L e u A l a
A A A C T A A G A G C T G G A A A A G C A T C A G A C T C A C A A A C C C C T G A T A C A A A A C C A G G A A A C A A A
L y s L e u A r g A l a G l y L y s A l a S e r A s p S e r G l n T h r P r o A s p T h r L y s P r o G l y A s n L y s
G C T G T T C C A G G T A A A G G T C A A G C A C C A C A A G C A G G T A C A A A A C C T A A C C A A A A C A A A G C A
A l a V a l P r o G l y L y s G l y G l n A l a P r o G l n A l a G l y T h r L y s P r o A s n G l n A s n L y s A l a
C C A A T G A A G G A A A C T A A G A G A C A G T T A C C A T C A A C A G G T G A A A C A G C T A A C C C A T T C T T C
P r o M e t L y s G l u T h r L y s A r g G l n L e u P r o S e r T h r G l y G l u T h r A l a A s n P r o P h e
A C A G C G G C A C G C G T T A C T G T T A T G G C A A C A G C T G G A G T A G C A G C A G T T G T A A A A C G C A A A
T h r A l a A l a A r g V a l T h r V a l M e t A l a T h r A l a G l y V a l A l a A l a V a l V a l L y s A r g L y s

FIG.7c

G A A G A A A A C T A A 1329
G l u G l u A s n > > > 443



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PROBE:

IgG



PROTEIN LG
PROTEIN L
PROTEIN G

Ig kappa



PROTEIN LG
PROTEIN L
PROTEIN G

IgG Fc



PROTEIN LG
PROTEIN L
PROTEIN G

16 kDa —
35 kDa —
50 kDa —

FIG. 8

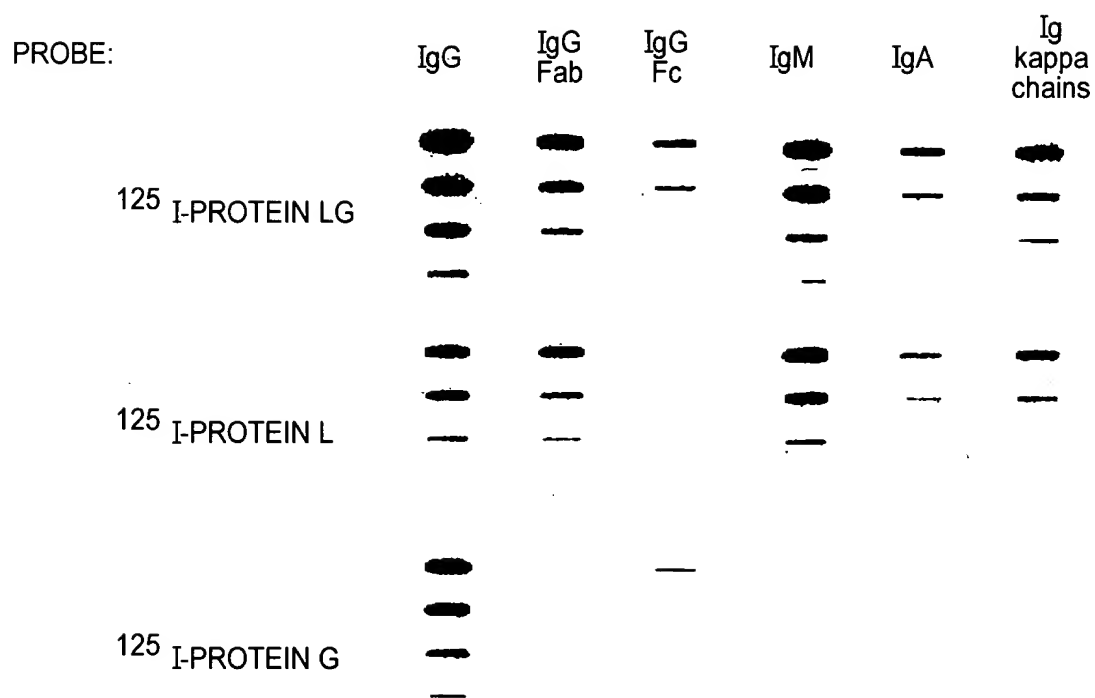
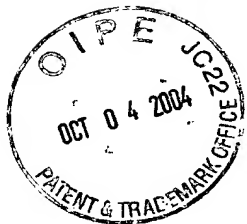


FIG. 9